



SEQUENCE LISTING

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HAGIWARA, Hiroko

<120> MARKER FOR SELECTING TRANSFORMANT WITH THE USE OF LETHAL GENE

<130> 040894-7170-US

<140> US 10/522,366

<141> 2005-01-25

<150> PCT/JP03/09543

<151> 2003-07-28

<150> JP 2002-218735

<151> 2002-07-26

<160> 24

<170> PatentIn version 3.4

<210> 1

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 1

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28

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57

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<223> Primer

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<220>
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gcatggccgc ctcggccgaa aggtttttaa gattacgggc atg 43

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<220>
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<400> 6
cgatgaattc tcaccaatca ccatcacgat aatc 34

<210> 7
<211> 598
<212> DNA
<213> Escherichia coli

<400> 7
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aaaactgaga atattaaagg gcttggtgat cttaagcctg ggataccaaa aacaccaaag 120

cagaatggtg gtggaaaacg caagcgctgg actggagata aagggcgtaa gatttatgag 180

tgggattctc agcatggtga gcttgagggg tatcgtgccg gtgatggtca gcatcttggc 240

tcatttgacc ctaaaacagg caatcagttg aaagggtccag atccgaaacg aaatatcaag 300

aaatatcttt gaggccatag cggccaagtt atgggactta aattggattt aacttggttt 360

gataaaagta cagaagattt taagggtagag gagtattcaa aagatttttg agatgacggt 420
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 gttatagctg aatgggtacc ttgctacaa ccatacttta atcatcaa attgatatttcc 540
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 <223> Primer

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<210> 9
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<400> 9
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<400> 10
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<400> 11
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<223> Primer

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<211> 58

<212> DNA

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<223> Primer

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<210> 14

<211> 607

<212> DNA

<213> Escherichia coli

<400> 14

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acaccaaagc agaatggtgg tggaaaacgc aagcgtgga ctggagataa agggcgtaag 180

atttatgagt gggattctca gcatggtgag cttgaggggt atcgtgccag tgatggtcag 240

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tgctttgatg ttatagctga atgggtacct ttgctacaac catactttta tcatcaaatt 540

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ttcatcg 607

<210> 15

<211> 258

<212> DNA

<213> Escherichia coli

<400> 15

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gagtattcaa aagatTTTgg agatgacggT tcagttatgg aaagtctagg tgtgcctttt 120
aaggataatg ttaataacgg ttgctttgat gttatagctg aatgggtacc tttgctacaa 180
ccatacttta atcatcaaat tgatatttcc gataatgagt attttgtttc gtttgattat 240
cgtgatggTg attggtga 258

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<211> 3066
<212> DNA
<213> Escherichia coli

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cgatcg 3066

<210> 17
<211> 551
<212> PRT
<213> Escherichia coli

<400> 17

Met Ser Gly Gly Asp Gly Arg Gly His Asn Thr Gly Ala His Ser Thr
1 5 10 15

Ser Gly Asn Ile Asn Gly Gly Pro Thr Gly Leu Gly Val Gly Gly Gly
20 25 30

Ala Ser Asp Gly Ser Gly Trp Ser Ser Glu Asn Asn Pro Trp Gly Gly
35 40 45

Gly Ser Gly Ser Gly Ile His Trp Gly Gly Gly Ser Gly His Gly Asn
50 55 60

Gly Gly Gly Asn Gly Asn Ser Gly Gly Gly Ser Gly Thr Gly Gly Asn
65 70 75 80

Leu Ser Ala Val Ala Ala Pro Val Ala Phe Gly Phe Pro Ala Leu Ser
85 90 95

Thr Pro Gly Ala Gly Gly Leu Ala Val Ser Ile Ser Ala Gly Ala Leu
100 105 110

Ser Ala Ala Ile Ala Asp Ile Met Ala Ala Leu Lys Gly Pro Phe Lys
115 120 125

Phe Gly Leu Trp Gly Val Ala Leu Tyr Gly Val Leu Pro Ser Gln Ile
130 135 140

Ala Lys Asp Asp Pro Asn Met Met Ser Lys Ile Val Thr Ser Leu Pro
145 150 155 160

Ala Asp Asp Ile Thr Glu Ser Pro Val Ser Ser Leu Pro Leu Asp Lys
165 170 175

Ala Thr Val Asn Val Asn Val Arg Val Val Asp Asp Val Lys Asp Glu
180 185 190

Arg Gln Asn Ile Ser Val Val Ser Gly Val Pro Met Ser Val Pro Val
195 200 205

Val Asp Ala Lys Pro Thr Glu Arg Pro Gly Val Phe Thr Ala Ser Ile
210 215 220

Pro Gly Ala Pro Val Leu Asn Ile Ser Val Asn Asn Ser Thr Pro Ala
225 230 235 240

Val Gln Thr Leu Ser Pro Gly Val Thr Asn Asn Thr Asp Lys Asp Val
245 250 255

Arg Pro Ala Gly Phe Thr Gln Gly Gly Asn Thr Arg Asp Ala Val Ile
260 265 270

Arg Phe Pro Lys Asp Ser Gly His Asn Ala Val Tyr Val Ser Val Ser
275 280 285

Asp Val Leu Ser Pro Asp Gln Val Lys Gln Arg Gln Asp Glu Glu Asn
290 295 300

Arg Arg Gln Gln Glu Trp Asp Ala Thr His Pro Val Glu Ala Ala Glu
305 310 315 320

Arg Asn Tyr Glu Arg Ala Arg Ala Glu Leu Asn Gln Ala Asn Glu Asp
325 330 335

Val Ala Arg Asn Gln Glu Arg Gln Ala Lys Ala Val Gln Val Tyr Asn
340 345 350

Ser Arg Lys Ser Glu Leu Asp Ala Ala Asn Lys Thr Leu Ala Asp Ala
355 360 365

Ile Ala Glu Ile Lys Gln Phe Asn Arg Phe Ala His Asp Pro Met Ala
370 375 380

Gly Gly His Arg Met Trp Gln Met Ala Gly Leu Lys Ala Gln Arg Ala
385 390 395 400

Gln Thr Asp Val Asn Asn Lys Gln Ala Ala Phe Asp Ala Ala Ala Lys
405 410 415

Glu Lys Ser Asp Ala Asp Ala Ala Leu Ser Ser Ala Met Glu Ser Arg
420 425 430

Lys Lys Lys Glu Asp Lys Lys Arg Ser Ala Glu Asn Asn Leu Asn Asp
435 440 445

Glu Lys Asn Lys Pro Arg Lys Gly Phe Lys Asp Tyr Gly His Asp Tyr
450 455 460

His Pro Ala Pro Lys Thr Glu Asn Ile Lys Gly Leu Gly Asp Leu Lys
465 470 475 480

Pro Gly Ile Pro Lys Thr Pro Lys Gln Asn Gly Gly Gly Lys Arg Lys
485 490 495

Arg Trp Thr Gly Asp Lys Gly Arg Lys Ile Tyr Glu Trp Asp Ser Gln
500 505 510

His Gly Glu Leu Glu Gly Tyr Arg Ala Ser Asp Gly Gln His Leu Gly
515 520 525

Ser Phe Asp Pro Lys Thr Gly Asn Gln Leu Lys Gly Pro Asp Pro Lys
530 535 540

Arg Asn Ile Lys Lys Tyr Leu
545 550

<210> 18
<211> 110
<212> PRT
<213> Escherichia coli

<400> 18

Ala Glu Asn Asn Leu Asn Asp Glu Lys Asn Lys Pro Arg Lys Gly Phe
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Lys Asp Tyr Gly His Asp Tyr His Pro Ala Pro Lys Thr Glu Asn Ile
20 25 30

Lys Gly Leu Gly Asp Leu Lys Pro Gly Ile Pro Lys Thr Pro Lys Gln
35 40 45

Asn Gly Gly Gly Lys Arg Lys Arg Trp Thr Gly Asp Lys Gly Arg Lys
50 55 60

Ile Tyr Glu Trp Asp Ser Gln His Gly Glu Leu Glu Gly Tyr Arg Ala
65 70 75 80

Ser Asp Gly Gln His Leu Gly Ser Phe Asp Pro Lys Thr Gly Asn Gln
85 90 95

Leu Lys Gly Pro Asp Pro Lys Arg Asn Ile Lys Lys Tyr Leu
100 105 110

<210> 19
<211> 97
<212> PRT
<213> Escherichia coli

<400> 19

Lys Gly Phe Lys Asp Tyr Gly His Asp Tyr His Pro Ala Pro Lys Thr
1 5 10 15

Glu Asn Ile Lys Gly Leu Gly Asp Leu Lys Pro Gly Ile Pro Lys Thr
20 25 30

Pro Lys Gln Asn Gly Gly Gly Lys Arg Lys Arg Trp Thr Gly Asp Lys
35 40 45

Gly Arg Lys Ile Tyr Glu Trp Asp Ser Gln His Gly Glu Leu Glu Gly
50 55 60

Tyr Arg Ala Ser Asp Gly Gln His Leu Gly Ser Phe Asp Pro Lys Thr
65 70 75 80

Gly Asn Gln Leu Lys Gly Pro Asp Pro Lys Arg Asn Ile Lys Lys Tyr
85 90 95

Leu

<210> 20
<211> 330
<212> DNA
<213> Escherichia coli

<400> 20
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 caaagcagaa tgggtggtgga aaacgcaagc gctggactgg agataaaggg cgtaagattt 180
 atgagtggga ttctcagcat ggtgagcttg aggggtatcg tgccagtgat ggtcagcatc 240
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 tcaagaaata tctttgaggc catagcggcc 330

<210> 21
 <211> 60
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic single-stranded oligonucleotide

<400> 21
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<210> 22
 <211> 60
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic single-stranded oligonucleotide

<400> 22
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<210> 23
 <211> 650
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 23
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 gctactctcc caaaaccaa aggtctccgc tgactagggc acatctgaca gaagtggaat 180
 caaggctaga aagactggaa cagctatttc tactgatttt tctcagagaa gaccttgaca 240
 tgattttgaa aatggattct ttacaggata taaaagcatt gttaacagga ttatttgtac 300
 aagataatgt gaataaagat gccgtcacag atagattggc ttcagtggag actgatatgc 360

ctctaacatt gagacagcat agaataagtg cgacatcatc atcggaagag agtagtaaca	420
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ttccgttgga ttttatgccc agggatgctc ttcattgatt tgattggtct gaagaggatg	540
acatgtcgga tggcttgccc ttctgaaaa cggaccccaa caataatggg ttctttggcg	600
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<210> 24
 <211> 535
 <212> DNA
 <213> *Aspergillus oryzae*

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tttttgttac ggtagccatg acccctccat ggcaaagaga gaggaggacg aggacgatca	180
ggaaactgtg tctcgccgct ataccacaat cgtgttatcc tgattgacat cttcttaaat	240
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